

# SCORE Search Results Details for Application 10828332 and Search Result us-10-828-332-6.rnpm.

[Score Home](#)    [Retrieve Application](#)    [SCORE System](#)    [SCORE](#)    [Comments /](#)  
[Page](#)    [List](#)    [Overview](#)    [FAQ](#)    [Suggestions](#)

This page gives you Search Results detail for the Application 10828332 and Search Result us-10-828-332-6.rnpm.

start

[Go Back to previous page](#)

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2006, 03:25:21 ; Search time 10101 Seconds  
(without alignments)  
9606.645 Million cell updates/sec

Title: US-10-828-332-6  
Perfect score: 1755  
Sequence: 1 atgccaggggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_Main:\*

- 1: /cgn2\_6/ptodata/1/pna/PCTUSA\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pna/PCTUSB\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pna/PCTUSC\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pna/US06\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pna/US075\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pna/US076\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pna/US077\_COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pna/US078\_COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pna/US079\_COMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pna/US080\_COMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq:\*

# SCORE Search Results Details for Application 10828332 and Search Result us-10-828-332-6.rnpn.

|                            |                                      |                              |                       |                             |
|----------------------------|--------------------------------------|------------------------------|-----------------------|-----------------------------|
| <a href="#">Score Home</a> | <a href="#">Retrieve Application</a> | <a href="#">SCORE System</a> | <a href="#">SCORE</a> | <a href="#">Comments /</a>  |
| <a href="#">Page</a>       | <a href="#">List</a>                 | <a href="#">Overview</a>     | <a href="#">FAQ</a>   | <a href="#">Suggestions</a> |

This page gives you Search Results detail for the Application 10828332 and Search Result us-10-828-332-6.rnpn.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: April 26, 2006, 03:27:02 ; Search time 722 Seconds  
(without alignments)  
7897.181 Million cell updates/sec

Title: US-10-828-332-6  
Perfect score: 1755  
Sequence: 1 atgccaggggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7549803 seqs, 1624434298 residues

Total number of hits satisfying chosen parameters: 15099606

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*

- 1: /SIDS5/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*
- 2: /SIDS5/ptodata/1/pna/US06\_NEW\_COMB.seq:\*
- 3: /SIDS5/ptodata/1/pna/US07\_NEW\_COMB.seq:\*
- 4: /SIDS5/ptodata/1/pna/US08\_NEW\_COMB.seq:\*
- 5: /SIDS5/ptodata/1/pna/US09\_NEW\_COMB.seq:\*
- 6: /SIDS5/ptodata/1/pna/US10\_NEW\_COMB.seq:\*
- 7: /SIDS5/ptodata/1/pna/US10\_NEW\_COMB.seq1:\*
- 8: /SIDS5/ptodata/1/pna/US11\_NEW\_COMB.seq:\*
- 9: /SIDS5/ptodata/1/pna/US11\_NEW\_COMB.seq1:\*
- 10: /SIDS5/ptodata/1/pna/US11\_NEW\_COMB.seq2:\*
- 11: /SIDS5/ptodata/1/pna/US11\_NEW\_COMB.seq3:\*
- 12: /SIDS5/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## EAST Search History

| Ref # | Hits | Search Query              | DBs                            | Default Operator | Plurals | Time Stamp       |
|-------|------|---------------------------|--------------------------------|------------------|---------|------------------|
| L1    | 3    | gabriel near ana          | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 09:04 |
| L2    | 1    | gabriel near san near ana | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 08:44 |
| L3    | 1809 | gabriel near san          | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 08:44 |
| L4    | 6    | maekawa near takami       | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 09:04 |
| L5    | 14   | uneyama near hisayuki     | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 09:05 |
| L6    | 17   | l1 or l2 or l4 or l5      | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 09:05 |
| L7    | 6    | l6 and glutamic           | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 09:08 |
| L8    | 5029 | glutamic adj acid.clm.    | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 09:08 |
| L9    | 390  | l8 and receptor.clm.      | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 09:10 |
| L10   | 14   | l9 and metabotrop\$3      | US-PGPUB;<br>USPAT;<br>DERWENT | OR               | ON      | 2006/10/02 09:10 |

=> d his

(FILE 'HOME' ENTERED AT 09:13:08 ON 02 OCT 2006)

FILE 'MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:13:26 ON 02 OCT 2006

L1 20033 S METABOTROP?  
L2 18304 S L1 (P) GLUTAM?  
L3 18203 S L2 (P) RECEPTOR  
L4 0 S L3 AND GABRIEL  
L5 17057 S L3 AND GLUTAMATE (1W) RECEPTOR  
L6 17003 S L5 AND METABOTROPIC  
L7 9227 DUP REM L6 (7776 DUPLICATES REMOVED)  
L8 0 S L7 AND PU<2000  
L9 4049 S L7 AND PY<2000  
L10 2654 S L9 AND PY>1995  
L11 743 S L10 AND PY>1998  
L12 0 S L11 AND SEQ NEAR ID  
L13 67 S L11 AND SEQUENCE  
L14 10 S L13 AND MRNA  
E GABRIEL ANA S /AU  
E GABRIEL SAN /AU  
E MAEKAWA TAKAMI /AU  
E UNEYAMA HISAYUKI /AU  
L15 14284 S E 3  
E MAEKAWA TAKAMI /AU  
L16 17 S E3  
L17 1 S L16 AND GLUTAMIC

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 25, 2006, 12:46:23 ; Search time 160.3 Seconds  
(without alignments)  
3025.990 Million cell updates/sec

Title: US-10-828-332-6  
Perfect score: 3303  
Sequence: 1 atgccagggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 15722378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10828332/runat\_25042006\_092247\_27363/app\_query.fasta\_1  
-DB=Pending\_Patents\_AA\_Main -QFMT=fastan -SUFFIX=rapm -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss02p -USER=US10828332\_@CGN\_1\_1\_1104\_@runat\_25042006\_092247\_27363  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending\_Patents\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/paa/US066\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/paa/US073\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/paa/US074\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/paa/US075\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/paa/US076\_COMB.pep:\*
- 7: /cgn2\_6/ptodata/1/paa/US077\_COMB.pep:\*
- 8: /cgn2\_6/ptodata/1/paa/US078\_COMB.pep:\*
- 9: /cgn2\_6/ptodata/1/paa/US079\_COMB.pep:\*
- 10: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep:\*
- 11: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep:\*
- 12: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep:\*

13: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep:\*  
 14: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*  
 15: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep:\*  
 16: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep:\*  
 17: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep:\*  
 18: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep:\*  
 19: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep:\*  
 20: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*  
 21: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep:\*  
 22: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep:\*  
 23: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep:\*  
 24: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep:\*  
 25: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep:\*  
 26: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*  
 27: /cgn2\_6/ptodata/1/paa/US097\_COMB.pep:\*  
 28: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*  
 29: /cgn2\_6/ptodata/1/paa/US099\_COMB.pep:\*  
 30: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*  
 31: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*  
 32: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
 33: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*  
 34: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep:\*  
 35: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep:\*  
 36: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep:\*  
 37: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep:\*  
 38: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep:\*  
 39: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep:\*  
 40: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep:\*  
 41: /cgn2\_6/ptodata/1/paa/US111\_COMB.pep:\*  
 42: /cgn2\_6/ptodata/1/paa/US112\_COMB.pep:\*  
 43: /cgn2\_6/ptodata/1/paa/US114\_COMB.pep:\*  
 44: /cgn2\_6/ptodata/1/paa/US600\_COMB.pep:\*  
 45: /cgn2\_6/ptodata/1/paa/US601\_COMB.pep:\*  
 46: /cgn2\_6/ptodata/1/paa/US602\_COMB.pep:\*  
 47: /cgn2\_6/ptodata/1/paa/US603\_COMB.pep:\*  
 48: /cgn2\_6/ptodata/1/paa/US604\_COMB.pep:\*  
 49: /cgn2\_6/ptodata/1/paa/US605\_COMB.pep:\*  
 50: /cgn2\_6/ptodata/1/paa/US606\_COMB.pep:\*  
 51: /cgn2\_6/ptodata/1/paa/US607\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result<br>No. | Score  | %     |              | DB | ID                  | Description       |
|---------------|--------|-------|--------------|----|---------------------|-------------------|
|               |        | Query | Match Length |    |                     |                   |
| 1             | 3107   | 94.1  | 584          | 38 | US-10-828-332-7     | Sequence 7, Appli |
| 2             | 3050.5 | 92.4  | 912          | 32 | US-10-219-051B-4035 | Sequence 4035, Ap |
| 3             | 3050.5 | 92.4  | 912          | 32 | US-10-219-051B-4039 | Sequence 4039, Ap |
| 4             | 3004.5 | 91.0  | 704          | 39 | US-10-932-333-1999  | Sequence 1999, Ap |
| 5             | 3004.5 | 91.0  | 704          | 49 | US-60-500-315-1999  | Sequence 1999, Ap |
| 6             | 3004.5 | 91.0  | 909          | 26 | US-09-679-664-48    | Sequence 48, Appl |
| 7             | 3004.5 | 91.0  | 912          | 1  | PCT-US04-00750-66   | Sequence 66, Appl |
| 8             | 3004.5 | 91.0  | 912          | 18 | US-08-816-178A-2    | Sequence 2, Appli |

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: April 25, 2006, 12:46:47 ; Search time 20.5 Seconds  
(without alignments)  
2553.097 Million cell updates/sec

Title: US-10-828-332-6  
Perfect score: 3303  
Sequence: 1 atgccaggggtatcatcatc.....acaccaaccatgccatctag 1755

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 629085 seqs, 149112515 residues

Total number of hits satisfying chosen parameters: 1258170

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10828332/runat\_25042006\_092249\_27375/app\_query.fasta\_1  
-DB=Pending\_Patents\_AA\_New -QFMT=fastan -SUFFIX=rapn -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss02p -USER=US10828332\_@CGN\_1\_1\_107\_@runat\_25042006\_092249\_27375  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending\_Patents\_AA\_New:\*  
1: /SIDS5/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /SIDS5/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /SIDS5/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /SIDS5/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /SIDS5/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /SIDS5/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /SIDS5/ptodata/1/paa/US11\_NEW\_COMB.pep:\*  
8: /SIDS5/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | %   |        | Query |        | DB | ID                   | Description       |
|--------|-----|--------|-------|--------|----|----------------------|-------------------|
|        | No. | Score  | Match | Length |    |                      |                   |
|        | 1   | 2219   | 67.2  | 915    | 8  | US-60-732-162-1552   | Sequence 1552, Ap |
|        | 2   | 2210   | 66.9  | 915    | 6  | US-11-344-728-2      | Sequence 2, Appli |
|        | 3   | 2191.5 | 66.3  | 922    | 8  | US-60-732-162-1554   | Sequence 1554, Ap |
|        | 4   | 2189   | 66.3  | 913    | 8  | US-60-732-162-1556   | Sequence 1556, Ap |
|        | 5   | 2054   | 62.2  | 877    | 6  | US-11-214-063A-1132  | Sequence 1132, Ap |
|        | 6   | 1284.5 | 38.9  | 1520   | 6  | US-11-214-063A-630   | Sequence 630, App |
|        | 7   | 1283   | 38.8  | 364    | 6  | US-11-293-697-4612   | Sequence 4612, Ap |
|        | 8   | 1131   | 34.2  | 1194   | 6  | US-10-567-867-636    | Sequence 636, App |
|        | 9   | 1131   | 34.2  | 1194   | 8  | US-60-751-420-1596   | Sequence 1596, Ap |
|        | 10  | 1123   | 34.0  | 1180   | 1  | PCT-US06-13172-7     | Sequence 7, Appli |
|        | 11  | 1123   | 34.0  | 1180   | 8  | US-60-742-219-2500   | Sequence 2500, Ap |
|        | 12  | 1121.5 | 34.0  | 878    | 7  | US-11-404-939-347    | Sequence 347, App |
|        | 13  | 1113   | 33.7  | 1199   | 6  | US-11-271-139-2      | Sequence 2, Appli |
| c      | 14  | 873    | 26.4  | 297    | 6  | US-10-498-451-1262   | Sequence 1262, Ap |
|        | 15  | 528    | 16.0  | 297    | 7  | US-11-360-355-120729 | Sequence 120729,  |
|        | 16  | 521    | 15.8  | 684    | 7  | US-11-360-355-120999 | Sequence 120999,  |
|        | 17  | 428.5  | 13.0  | 839    | 8  | US-60-751-420-42     | Sequence 42, Appl |
|        | 18  | 427.5  | 12.9  | 879    | 6  | US-11-214-063A-454   | Sequence 454, App |
|        | 19  | 426.5  | 12.9  | 929    | 6  | US-11-214-063A-868   | Sequence 868, App |
|        | 20  | 359.5  | 10.9  | 936    | 6  | US-11-214-063A-602   | Sequence 602, App |
|        | 21  | 313.5  | 9.5   | 371    | 7  | US-11-360-355-120501 | Sequence 120501,  |
|        | 22  | 299    | 9.1   | 4315   | 6  | US-10-461-673-9612   | Sequence 9612, Ap |
|        | 23  | 282.5  | 8.6   | 595    | 8  | US-60-742-219-2100   | Sequence 2100, Ap |
|        | 24  | 282.5  | 8.6   | 755    | 6  | US-11-214-063A-450   | Sequence 450, App |
|        | 25  | 277.5  | 8.4   | 413    | 7  | US-11-056-355B-4735  | Sequence 4735, Ap |
|        | 26  | 271    | 8.2   | 7285   | 6  | US-11-272-521-28     | Sequence 28, Appl |
|        | 27  | 265    | 8.0   | 493    | 7  | US-11-056-355B-65494 | Sequence 65494, A |
|        | 28  | 262    | 7.9   | 375    | 7  | US-11-056-355B-3621  | Sequence 3621, Ap |
|        | 29  | 261.5  | 7.9   | 519    | 7  | US-11-056-355B-6752  | Sequence 6752, Ap |
|        | 30  | 259.5  | 7.9   | 487    | 7  | US-11-056-355B-6753  | Sequence 6753, Ap |
|        | 31  | 258.5  | 7.8   | 3682   | 7  | US-11-174-307B-2486  | Sequence 2486, Ap |
|        | 32  | 251.5  | 7.6   | 2757   | 7  | US-11-174-307B-1642  | Sequence 1642, Ap |
|        | 33  | 249.5  | 7.6   | 502    | 6  | US-10-461-673-12610  | Sequence 12610, A |
|        | 34  | 247    | 7.5   | 4440   | 6  | US-10-184-614A-525   | Sequence 525, App |
|        | 35  | 247    | 7.5   | 4440   | 6  | US-10-184-615A-525   | Sequence 525, App |
|        | 36  | 245.5  | 7.4   | 1659   | 7  | US-11-174-307B-3184  | Sequence 3184, Ap |
|        | 37  | 243    | 7.4   | 2118   | 6  | US-11-192-046-125    | Sequence 125, App |
|        | 38  | 243    | 7.4   | 2578   | 6  | US-10-244-081A-31    | Sequence 31, Appl |
|        | 39  | 242.5  | 7.3   | 1269   | 7  | US-11-174-307B-164   | Sequence 164, App |
|        | 40  | 242.5  | 7.3   | 1356   | 7  | US-11-174-307B-64    | Sequence 64, Appl |
|        | 41  | 242    | 7.3   | 291    | 7  | US-11-056-355B-3800  | Sequence 3800, Ap |
|        | 42  | 241.5  | 7.3   | 3259   | 7  | US-11-174-307B-1020  | Sequence 1020, Ap |
|        | 43  | 241.5  | 7.3   | 3259   | 7  | US-11-174-307B-2622  | Sequence 2622, Ap |
|        | 44  | 241.5  | 7.3   | 4243   | 7  | US-11-174-307B-1722  | Sequence 1722, Ap |
|        | 45  | 241    | 7.3   | 473    | 1  | PCT-US06-07136-166   | Sequence 166, App |

## ALIGNMENTS

RESULT 1

US-60-732-162-1552